

Serial No. 09/927,161  
Page 5

#### APPENDIX I

#### CLEAN VERSION OF THE ENTIRE SET OF PENDING CLAIMS AS AMENDED IN THIS COMMUNICATION

The following is a list of the Claims as they would appear following entry of this amendment.

1. (original) A method of producing a transformed microorganism, comprising:
  - (i) selecting a competent microorganism;
  - (ii) producing a DNA construct *in vitro*; and
  - (iii) directly transforming said microorganism with said DNA construct such that the DNA construct becomes integrated into a chromosome of said microorganism.
2. (currently amended) The method of claim 1, wherein said microorganism is selected from the group consisting of ~~Acinetobacter, Thermus, Deinococcus, Radiodurans and Bacillus~~ Acinetobacter, Thermus, Deinococcus, Radiodurans and Bacillus.
3. (currently amended) The method of claim 2, wherein said microorganism is a Bacillus ~~Bacillus~~.
4. (currently amended) The method of claim 3, wherein said Bacillus ~~Bacillus~~ is a super-competent strain.
5. (currently amended) The method of claim 4, wherein said super-competent Bacillus ~~Bacillus~~ is a P<sub>xyl</sub>-comK strain.
6. (original) The method of claim 1, wherein said DNA construct comprises homologous DNA selected from the group consisting of wild-type, mutagenized and modified DNA.
7. (original) The method of claim 1, wherein said DNA construct comprises heterologous DNA selected from the group consisting of wild-type, mutagenized and modified DNA.

Serial No. 09/927,161

Page 6

8. (currently amended) The method of claim 1, wherein said DNA construct comprises an incoming sequence ~~sequence~~ of interest, flanked on each side by a homology box.

9. (original) The method of claim 8, wherein said DNA construct further comprises stuffer sequences.

10. (original) The method of claim 1, wherein said DNA construct is a non-plasmid DNA construct.

11. (original) The method of claim 1 wherein the DNA construct is produced without the use of a shuttle vector or an intermediate host.

12. (original) The method of claim 1, further comprising the steps of selecting a target sequence in a chromosome of said competent microorganism, and increasing the homology between said target sequence and said DNA construct.